

- Cupina T, Borojevic S, and Janjatovic V. 1981. Chlorophyll content and mesophyll thickness in the green parts of different cultivars of wheat. *Field Crops Abstr* 34: 3050.
- Hahn GM and Li GC. 1990. Thermotolerance, thermoresistance, and thermosensitization. *In: Stress proteins in biology and medicine* (Morimoto RI, Tissieres A, and Georgopoulos C Eds). Cold Spring Harbor Press, Cold Spring Harbor, New York, pp 79-100.
- Howard A. 1924. *Crop production in India: a critical survey of its problems*. Oxford University Press, UK. 200 pp.
- Sharma A. 2006. Genetic and physiological studies for heat tolerance in bread wheat (*Triticum aestivum* L. em. Thell.). M.Sc.Ag. Thesis (Genetics and Plant Breeding), G.B. Pant Univ of Agric and Tech, Pantnagar, U.S. Nagar, India.
- Joshi CP, Klueva NY, Morrow KJ, and Nguyen HT. 1997. Expression of a unique plastid-localized heat-shock protein is genetically linked to acquired thermo-tolerance in wheat. *Theor Appl Genet* 95:834-841.
- Nguyen HT, Hendershot KL, and Joshi CP. 1992. Molecular genetics for stress breeding: heat-shock proteins. *In: Proc Internat Crop Sci Cong I* (Buxton DR, Shibles R, Forsberg RA, Blad BL, Asay KH, Paulsen GM, and Wilson RF, Eds). Crop Science Society of America, Madison, WI, pp. 541-554.
- Vierling E. 1991. The roles of heat-shock proteins in plants. *Ann Rev Plant Physiol Plant Mol Biol* 42:579-620.

INDIAN AGRICULTURAL RESEARCH INSTITUTE (IARI)
Regional Station, Wellington, The Nilgiris (T.N.) – 643231, India.

Performance of brown and black rust resistance genes in some wheat cultivars of central, peninsular, and south India.

J. Kumar, M. Sivasamy, and R. Nisha.

Some of the popular wheat cultivars grown in central, peninsular, and southern India were evaluated for seedling and adult-plant resistance to black and brown rusts. Because the source of rust inoculum for Central and Peninsular India lies mainly in Nilgiri Hills in southern India, the cultivars were tested only with Nilgiri pathotypes. Cultivars were raised as single lines in plastic trays (12 x 5 cm) each accommodating 10 lines (8 seedlings/line). Uredospore dust of individual pathotypes prevailing in the Nilgiri Hills and maintained artificially at the IARI Regional Station, Wellington, was inoculated on the wet surface of the primary leaves of 7-day-old seedlings of the test cultivars by a uniform rub application from base to tip. Inoculated pots were kept in a fine mist created with a manually operated water sprayer making a free film of water on the leaf surface. The plants were kept in a high humidity atmosphere maintained in glass humidity chambers. After 24 hours, the pots were transferred to benches in the glasshouse. Optimum temperature (20°C for brown and 25°C for black rust) and a light regime of 16:8 hours light:dark cycle maintained in the glass houses permitted full expression of brown and black rust pustules after 12 days. Host-pathogen interactions were recorded by following standard international procedures of Johnston and Mains (1932) in brown rust and Stackman and Levine (1922) in black rust. Cultivars also were sown in an open field environment exposing them to natural rust pathotypes prevailing in Wellington to evaluate adult-plant resistance response. Rust intensities were recorded on these cultivars at growth stage 71 (Zadoks et al. 1974) following the Peterson scale (Peterson et al. 1948) for estimating adult-plant resistance.

Seedling and adult-plant response of cultivars are given in Table 1 (p. 81). In the Central Zone, seven of eight tested cultivars exhibited seedling resistance to all the pathotypes of brown and black rust prevalent in the Nilgiri Hills. These seven cultivars were HI 8498, HI 8381, HI 1544, HI 1531, HI 8627, DL 788-2, and HD 4672 were free of infection from brown and black rusts at the adult stage; their field resistance is robust only if the inoculum in central India originates from the Nilgiri Hills. Only cultivar HI 1500 of central India showed susceptibility but that was only to one race 77-5 (121R63-1) of brown rust. Fortunately, this genotype has strong adult-plant resistance to brown rust (0 rating). Partial susceptibility (10S) of HI 1500 to black rust is a very positive feature because such incomplete resistance restricts the epiphytotic development of disease so that economic losses do not exceed the threshold (field durability; Parlevliet 1977). The majority of the cultivars of the Central Zone possess gene *Sr2*, which is quite desirable for the purpose of preventing black rust epidemics in this zone. Because of the presence of *Sr2*, the rust resistance seems to be stable in the Central Zone even after 4–5 decades of utilization of the cultivars possessing this gene. This gene is derived from the cultivar Hope, which is responsible for reducing yield losses to only negligible amounts since the late 1960s in

Table 1. Response of popular wheat cultivars of the Central, Peninsular, and South Hill Zones to individual pathotypes at the seedling stage and to a mixture of pathotypes at the adult-plant stage of brown, black, and yellow rusts.

Cultivar	Seedling reaction						Adult-plant reaction		Seedling resistance genes present		
	Brown rust pathotypes				Black rust pathotypes		Brown rust	Black rust	Black rust	Brown rust	Yellow rust
	77A	77-5	77-7	77-8	40A	40-1					
Central Zone											
HI 8498	;	;1	;1	;1	;	0	0	0	<i>Sr2</i>	<i>Lr23</i>	—
HI 8381	;2	;1	;2	;1	;2+	2+	0	0	<i>Sr2+Sr9e</i>	—	—
HI 1544	;2	0;	;1	;1	;1	;1	0	0	<i>Sr2</i>	—	—
HI 1531	;2	;2	;2	;2	;	;	0	0	<i>Sr2+Sr24</i>	<i>Lr24</i>	—
HI 8627	;1	;1	;1	;1	;	0	0	0	<i>Sr9e</i>	—	—
DL 788-2	;1	;1	1	0;1	;	0	0	0	<i>Sr2+Sr5+Sr24</i>	<i>Lr24</i>	—
HD 4672	;2	;2	;1	;1	;1	1	0	0	—	<i>Lr23</i>	—
HI 1500	;1	3+	;2	;2+	;12+	;	0	10S	—	—	—
Peninsular Zone											
Raj 4037	2	3+	2+	;2	2+	2+	80S	20S	<i>Sr2</i>	—	—
DWR 162	2+	3+	2+	2+	2	2	60S	10MR	<i>Sr2+Sr31</i>	<i>Lr23+Lr26</i>	<i>Yr9</i>
MACS 2496	2+	3+	2+	22+	2	1	40S	10MR MS	<i>Sr2+Lr31</i>	<i>Lr1+Lr23+Lr26</i>	<i>Yr9</i>
DDK 1001	;2	0;	;	;1	0;	;1	0	0	—	—	—
DDK1009	;1	;2	;2	;2	;	2	0	0	—	—	—
NIAW 917	0;	0;	0	0;	;1	0	0	0	<i>Sr2+Sr31</i>	<i>Lr26</i>	<i>Yr9</i>
DDK 1025	;2	;1	;1	0;	;	;	0	0	—	—	—
UAS 415	;2	;12	;1	;2	1	;	0	0	—	<i>Lr23</i>	—
DWR 195	2+	3+	2+	2+	0;1	2	20S	20MS	<i>Sr2+Sr31</i>	<i>Lr1+Lr23+Lr26</i>	<i>Yr9</i>
NIAW 34	;2	;2	;2+	;2	;1	2+	60S	0	<i>Sr11</i>	<i>Lr13+Lr34</i>	<i>Yr18</i>
Raj 4083	2+	2+	2+	12+	;1	2	10S	0	—	<i>Lr23</i>	—
HD 2781	;1	;1	;1	;1	0	3+	0	0	<i>Sr2</i>	—	—
K9644	2+	2+	2+	2	0;	0	20S	0	<i>Sr2</i>	<i>Lr13</i>	—
MACS 1967	1	;2	2	2	2	2+	0	0	<i>Sr11</i>	—	—
AKDW 2997-16	;1	;2	;12	0;	1	;	0	0	—	—	—
Bijaga yellow	1	;1	;2	;2	;1	;	0	0	<i>Sr2+Sr11</i>	<i>Lr23</i>	—
South Hill Zone											
HW 1085	;1	;1	;1	0;1	0	0	0	0	<i>Sr24+Sr31</i>	<i>Lr24</i>	—
HW 2044	;1	;1	;2	;2	;1	;	0	0	<i>Sr2+Sr25</i>	<i>Lr19</i>	—
HW 2045	1	;1	;1	;1	0	0	0	0	<i>Sr2+Sr25</i>	<i>Lr19</i>	—
HW 3094	;2	;1	;	0;	0	;1	0	0	<i>Sr24+Sr31</i>	<i>Lr24+Lr26</i>	<i>Yr9</i>
HD 2833	22+	;1	;	;1	;1	;1	0	5MRMS	<i>Sr24</i>	<i>Lr24</i>	—
HW 3083	;	0;	;	0	0;	;2	0	0	—	—	—
HW 2000	;2	;1	;1	;1	;1	;	0	0	—	—	—
HW 5013	;2	;1	;1	0;	;1	;2	0	0	<i>Sr24+Sr31</i>	<i>Lr24+Lr26</i>	<i>Yr9</i>

South America. This resistance is based on the *Sr2* gene complex, which actually consists of *Sr2* plus 4–5 minor genes pyramided into 3–4 gene combinations (Rajaram et al. 1988). *Sr2* alone behaves as a slow-rusting gene. Because there have been no major stem rust epidemic in areas where CIMMYT germ plasm is grown worldwide, the resistance shows promise to be durable also in India. In addition to having *Sr2* protection against black rust, the two cultivars HI 1531 and DL 788-2 also possess *Lr24*, a gene currently resistant to all Indian pathotypes of brown rust and capable of providing simultaneous protection. Fortunately, the *Lr24* gene is present in combination with *Lr26* in cultivars HW 3094 and HW 5013 of the South Hill Zone (Table 1), which is an area of inoculum source. Such a combination may act as an

impediment to rising of new races. The presence of *Sr2* in a majority of cultivars of the Peninsular Zone (Table 1, p. 81) guarantees averting yield losses in this zone in the future because of the proven durability of this gene.

In the Peninsular Zone, 16 popular wheat cultivars were evaluated for seedling and adult-stage resistance and 11, DDK 1001, DDK 1009, NIAW 917, DDK 1025, UAS 415, NIAW 34, Raj 4083, HD 2781, K 9644, MACS 1967, and AKDW 2997-16, showed excellent resistance to Nilgiri flora of black and brown rust pathogens at both the stages (Table 1, p. 81). Three cultivars, Raj 4037, DWR 162, and MACS 2496, were either completely or partially susceptible at seedling stage to brown rust and also susceptible to Nilgiri pathotypes of brown rust pathogen at the adult stage. Thus, the resistance of these three cultivars should be improved or they should be discouraged from cultivation if occupying large acreages in the states of Maharashtra and Karnataka. Nevertheless, these three cultivars need to be retained in the germ plasm pool because of their utility as partially resistant lines for black rust at the adult-plant stage. Such a trait makes these genotypes excellent genetic stocks for deriving durable resistance either for direct cultivation or for incorporation into other high-yielding but susceptible cultivars. Still another genotype, DWR 195, is susceptible to the most predominate pathotype 77-5 (121R63-1) but only at seedling stage. This cultivar holds promise, because it is resistant to black rust at the seedling stage and possesses excellent partial resistance to both black and brown rusts giving it potential to become a durably resistant cultivar in Peninsular India.

Seedling and adult-plant reaction of eight wheat cultivars released for cultivation in the Southern Hill Zone are given in Table 1 (p. 81). All exhibited high levels of resistance (≤ 2 as seedlings and 0–5MR as adult plants) to the Nilgiri flora of both brown and black rusts. In the Southern Hill Zone, wheat is cultivated only in a few thousand ha in the hilly areas of southern Karnataka and parts of Tamil Nadu (Jag Shoran et al. 2009). Because these are the areas where host–pathogen contact is maintained continuously and selection pressure can favor pathogen survival, new, virulent mutants can emerge if host cultivars have single, major genes. Regarding black rust resistance of cultivars released for the Southern Hill Zone, the situation is comfortable because the majority possess more than one gene making them suitable for cultivation in this zone without imminent danger of new pathogenic variants emerging. Brown rust resistance, however, is worrisome with some of the cultivars, e.g., HW 1085, HW 2044, HW 2045, and HD 2833, because they possess only single genes, either *Lr19* or *Lr24*. No virulence for gene *Lr24* is known in India (Mishra et al. 2001), but its singular presence HW 1085 and HD 2833, which are recommended for cultivation in the Southern Indian hills may contribute to new pathogenic mutants by virtue of year round culture. These new variants may not be so threatening for wheat cultivation in South Indian Hills because less area is under wheat cultivation, but they may become a potential constraint in production of *Lr24*-containing wheats such as HI 1531 and DL 788-2 in the Central Zone. Thus, pyramiding more genes in cultivars with *Lr24* grown in the Southern Hill Zone is needed so that they can be cultivated more safely in the rust source areas of hilly Tamil Nadu and southern Karnataka. Such multigenic complexes of rust resistance genes may curtail the arising of new pathogenic mutants.

References.

- Johnston CO and Mains EB. 1932. Studies on physiologic specialisation in *Puccinia triticiniae*. Tech Bull 313, USDA. 22 pp.
- Mishra AN, Roelfs AP, and Dubin HJ. 2001. Virulence for wheat leaf rust resistance gene *Lr24* in Nepal. Cereal Rusts and Powdery Mildews Bull (www.crpmb.org/2001/0920mishra).
- Parlevliet JE and Zadoks JC. 1977. The integrated concept of disease resistance: a new view including horizontal and vertical resistance in plants. Euphytica 26:5-21.
- Peterson RE, Campbell AB, and Hannah AE. 1948. A diagrammatic scale for estimating rust intensity of leaves and stems of cereals. Can J Res (C) 26:496-500.
- Rajaram S, Singh RP, and Toress E. 1988. Current CIMMYT approaches in breeding wheat for rust resistance. In: Breeding Strategies for resistance to the rusts of wheat (Simmonds NW and Rajaram S, Eds). CIMMYT, Mexico. Pp. 101-118.
- Shoran J, Singh G, Tyagi BS, and Singh SS. 2009. Wheat research in India: Past, Present and Future. In: Consolidating the productivity gain in wheat - an outlook (Sharma RK, Aggarwal R, Sharma AMSA, and Sharma JB, Eds). Proc 48th All India Wheat and Barley Research Workers Meet, IARI, New Delhi, 28-31 August. 119 pp.
- Stakman EC and Levine MN. 1922. The determination of biologic forms of *Puccinia graminis* on *Triticum* spp. Minn Agric Res Stn Bull 8:10.
- Zadoks JC, Chang TT, and Konzak CF. 1974. A decimal code for the growth stages of cereals. Eucarpia Bull 7:1-10.

Two new wheat cultivars, Pusa-Navagiri and CoW(SW)2, released for cultivation in the Southern Hill Zone and the nontraditional areas of South India.

M. Sivasamy, Jagdish Kumar, and V.K. Vikas, and A. Nirmala Kumari and N. Senthil (Department of Millets and CPMB&BT, Tamil Nadil Agricultural University, Coimbatore-3, India).

The two disease-resistant, heat-tolerant, high-yielding wheat cultivars developed at IARI, Regional Station, Wellington, were released for cultivation under conditions in the Southern Hill Zone of India. The bread wheat HW 5207 (Pusa Navagiri) was released through All India Co-ordinated Wheat Improvement Programme and a *T. turgidum* subsp. *dicoccum* (Samba) wheat cultivar named HW 1095 and also known as CoW(SW)2 was released by Tamil Nadu Agricultural University, Coimbatore, as a state variety for cultivation in the Southern Hill Zone.

The Southern Hills are known as the main foci for leaf and stem rust inoculum to the plains of India. Hence, the development of high-yielding, rust-resistant wheat cultivars and their saturation in these areas is of national importance in order to arrest the dissemination of uredospores to the plains of India.

In the Southern Hill Zone, wheat is not grown commonly except in the areas adjoining Western and Eastern Ghats, which covers some districts of the west and north Tamil Nadu and southern Karnataka states, because of very short winters and unfavorable conditions for cultivation. These areas also have comparatively high temperatures, and the crop is damaged from high infections of *Sclerotium* foot rot.

The agro-ecological conditions in the Southern Hill Zone, high altitudes prone to frost damage, midaltitudes with erratic monsoon, and low hills with frequent water shortages during the short winters, prompted us to develop the early maturing, thermo-tolerant, rust- and foot-rot resistant bread wheat genotype HW5207. This bread wheat fits well in the local crop rotation with wider adaptability. HW 5207 has a yield potential up to 5.96 t/ha under need-based/restricted irrigation (up to five irrigations) and exhibiting remarkable resistance to all three rusts. Because HW 5207 matures in 100–102 days, it could become a choice and alternative crop for the resource-poor farmers in the areas where erratic and unpredictable northeastern monsoons occur. HW 5207 consistently yields under varied levels of irrigation and has a 32.5% yield advantage over control cultivars under two irrigation levels. HW5207 will ensure both grain and fodder for sustaining the livelihood of resource-poor farmers.

Salient features of the proposed cultivar HW 5207.

- The genotype HW 5207 (Pusa navagiri) recorded the highest mean grain yield (52.1 q/ha) over the best check COW(W)1(48.75 q/ha) over the testing period. The superiority yield ranged from 7–18%.
- HW 5207 ranked in the first nonsignificant group eight out of 12 times (66.6%) over four years of testing at different locations indicating its wider adaptability and stability in its performance.
- HW 5207 exhibited a high degree of resistance to stem, leaf, and stripe rusts under both artificial and natural epidemic conditions against all the pathotypes occurring in the Nilgiris. The resistance to rusts and powdery mildew is attributed to the likely presence of a combination of genes, *Sr2* (based on the presence of pseudo-black chaff, tightly linked to *Sr2*), *Sr3J*, and *Sr24* for stem rust; *Lr24* and *Lr26* for leaf rust; *Yr9* and *Yr15* for yellow rust; and *Pm8* for powdery mildew. These genes likely were derived from the parents involved in the cross.
- HW 5207 yielded consistently higher over the best check HW 2044 when tested at more locations in areas adjoining the Nilgiri and Palani Nills and nontraditional areas, indicating its elasticity.
- HW 5207 recorded highest mean grain yield of 58.7 q/ha under two irrigation levels in trials as compared to the best check HW 2044. The over-all gain with two irrigations is 32.5%, which is the most favorable feature of the cultivar. The 12.1% advantage in mean yield obtained over HW 2044 under different irrigation levels indicates an ability for increased yield under varied soil moisture levels.
- HW 5207 has the ideal plant height (90 cm) with strong and resilient stems that provide resistance to lodging. The very nutritious grain registers 40.5 g mean test weight with > 11% protein and a high levels of iron (53.1 ppm), zinc (46.3 ppm), copper (5.33 ppm), and manganese (47.5 ppm) when compared to the checks indicating the nutritional quality of the grain it produces. In addition, HW 5207 has high scores for bread-making quality (7 out of 10), chapatti quality (7.42 out of 10), a *Glu-1* score of 8 out of 10, mean sedimentation value of 45.5, and a high hectolitre weight of 78.3 (kg/hl).

Cultivation of HW 5207 will provide an alternative to HW 2044 and Cow(w)1 and create additional genetic diversity to contain rust from the foci of rust inoculum and will have an added yield advantage as HW5207 shown better adaptability; suit cultivation in high altitudes, at middle elevations, and in lower hills as well as areas adjoining the hills; offer protection against the prevailing rusts and minor foliar diseases such as leaf blight, powdery mildew, and Sclerotium foot rot under field conditions; produce more grain (50 q/ha) along with fodder ensuring farm sustainability; and confer a high degree of resistance at field level in the zone, which could be attributed to the likely presence of *Lr24+Sr24*, *Sr31+Lr26+Yr9+Pm8*, and *Yr15* possibly derived from the parents involved in the cross, evidenced from the Seedling Response Test. In addition, the presence of prominent pseudo-black chaff, which is tightly linked to *Sr2* (a race nonspecific APR gene), in combination with other stem rust genes is expected to offer durable resistance against the most frequent pathotypes of rust in the Southern Hill Zone, a hot spot for foliar diseases of wheat in India.

Release of HW 1095, a semidwarf dicoccum as CoW(SW)2.

HW 1095, a semidwarf, disease-resistant, nutritionally rich, economically viable and high yielding dicoccum (Samba wheat) wheat developed at IARI, Regional Station, Wellington, using mutation techniques, is released for parts of Tamil Nadu and the Southern Hill Zone, including nontraditional areas, in collaboration with Tamil Nadu Agricultural University, Coimbatore, as state release. Wheat is one of the most important cereal crops in the world, ensuring food security to humankind. Although as many as 18 species of wheat were described and recognized by Percival (1921), only a few are of importance in agriculture. India is one of the very few countries in the world that cultivates all three important commercially cultivated species of wheat, *T. aestivum* subsp. *aestivum* (common bread or chappati wheat), *T. turgidum* subsp. *durum* (macaroni or durum wheat), and *T. turgidum* subsp. *dicoccum* (emmer, dicoccum, or Samba wheat). Bread wheat is the most important species accounting for a little over 87% of the total wheat production in India followed by durum (about 12%) and dicoccum (about 1%). Unlike *aestivum* and durum wheat, dicoccum wheat is grown on only limited acreage in Tamil Nadu, Karnataka, and parts of Maharashtra. Even today, a considerable area under dicoccum can be found in the northwestern Tamil Nadu, Karnataka, Maharashtra, and parts of Andhra Pradesh states. The farmers have preserved this wheat species because of its nutritional, nonshattering, and drought-tolerant traits. Currently, the tall land races that were released as NP 200, NP201, and NP 202, from IARI, Wellington, during 1960s are under cultivation in the southern Indian states for the traditional food preparation are made from dicoccum.

Incorporating dietary fiber-rich, dicoccum, whole-wheat flour in the regular diet of a diabetic significantly reduced total lipids ($p \leq 0.01$), triglycerides ($p \leq 0.01$), and LDL cholesterol ($p \leq 0.05$) (Yenagi N et al. 2001). Dicoccum wheat has therapeutic properties that can effectively reduce the cardiovascular risk factors. Managing diabetes, a life-long ailment, with medicine is very expensive and a dicoccum diet plays a crucial role in reducing the levels of plasma cholesterol and lowering glycemic response. The hulled grain of dicoccum wheat is used mainly in the alternative or health food markets. Most of the suggested beneficial effects of this cereal is from the specific characteristics of the fiber. Pyrolysis fragments derived from the polysaccharide fraction were significantly more abundant in dicoccum than in the other genotypes, whereas the highest percentage of lignin-derived pyrolysis fragments was detected in durum wheat. Results suggest that dicoccum genetic material may represent a source of high-value dietary fiber; dicoccum is much higher in fiber than common wheat. Future wheat-breeding programs should aim to preserve such characters.

In India, first three dicoccum cultivars, NP 200, NP 201, and NP 202, which were selected from Rishi Valley collections in Andhra Pradesh, were released for commercial cultivation during 1960s from the IARI Regional Station, Wellington. These cultivars are tall, tend to lodge, and are susceptible to yellow rust. Attempts were made to develop semidwarf dicoccum cultivars using dwarfing gene(s) derived from closely related tetraploid durum species, and a number of semidwarf cultivars were released from the University of Agricultural Sciences, Dharwad (DDK 1001, DDK 1009, DDK 1026, and DDK 1029) and from the Agharkar Research Institute, Pune. Although the dwarfing gene(s) derived from durum helped in developing semidwarf dicoccum wheats, most of them are now susceptible to yellow, particularly against pathotype 'I' (38S102) prevalent in the Southern Hills, and also produced undesirable end-product, grain traits, such as slightly sticky, reduced-quality fiber Rawa 'Uppuma', and were less preferred by the millers.

Therefore, a meticulously planned, dicoccum-improvement program was undertaken at IARI, Wellington, during 2002 for developing semidwarf dicoccum wheats without altering the quality of NP200, NP 201, and NP 202 by mutation breeding. Gamma irradiation of 10 (100 Gy (Gray is the unit of absorbed dose and is 1 Joule/kg)), 20 (200 Gy), 30 (300 Gy), and 40 (400 Gy) Kr γ -rays was given at optimal seed moisture levels. The irradiated seed were sown as M₁

and desirable plants were selected in the M² at 200 Gy dose. A stable population was fixed at M₄ that was entered into the All India Co-ordinated Trials as HW 1095 in 2005.

The salient features of HW 1095 (released as CoW(SW)2).

- dicoccum wheat HW 1095 developed at IARI, Regional Station, Wellington, is a NP200-mutant through gamma irradiation (200 Gray) maturing in 110 days, belonging to the early duration group.
- Culture HW 1095 recorded a mean grain yield of 4,040 kg/ha, which is an increase of 26% over NP 200 in a total of 98 trials over the past five years. NP 200 was used as a check. The yield of NP 200 was 3,190 kg/ha.
- Culture HW 1095 has 10–12 productive tillers with long and slightly tapering ears. A special attribute of this culture is the broad and waxy green foliage, drooping leaves, lodging resistance, and nonshattering grains. Rich in protein (13.2%) with a high sedimentation value (25), the reddish colored grain provides a good grain appearance and score of 8.
- The culture is resistant to black (stem), yellow (stripe), and brown (leaf) rusts. No major incidence of pests occurred in this Samba wheat culture. In view of a high and stable yield performance over locations and resistance to leaf and stem rust diseases, the culture HW 1095 is proposed for release as wheat CoW (SW) 2 in collaboration with Department of Millets, Tamil Nadu Agricultural University, Coimbatore, as state release.
- The released cultivar HW 1095-CoW(SW)2 was significantly superior in yield over NP 200 and DDK 1029 during the testing period.
- HW 1095 occurred 11/18 times in first nonsignificant group indicating wider adaptability and stability in performance across zones.

The release of this Samba wheat CoW(SW)2 is likely to boost the re-introduction of dicoccum wheat in the traditional dicoccum belt. In addition, resource-poor farmers will earn a better livelihood, because dicoccum grain garners a higher price in the market than other types of wheat. Our efforts at IARI, Wellington, now are to improve NP201 and NP202, and of these, one promising entry HW 1098 already has been entered in AICWIP Co-ordinated Trials.

References.

- Percival J. 1921. *The Wheat Plant*. Duckworth & Co, London, UK. 463 pp.
- Yenagi NB, Hanchinal RR, Patil CS, and Koppikar V. 2001. Glycemic and lipidemic response to dicoccum wheat (*Triticum dicoccum*) in the diet of diabetic patients. *Int J Diab Dev Ctries* 21:153-5.

A protein marker as a tool to detect the Secale cereale-derived linked genes Sr31, Lr26, Yr9, and Pm8 genes in wheat.

Rebekah Nisha, M. Sivasamy, Jagdish Kumar, and V.K. Vikas; K. Gajalakshmi and P. Shajitha (P.S.G.R Krishnammal College for Women, Coimbatore, India); and N. Senthil (Center for Plant Molecular Biology and Bio-technology, Tamil Nadu Agricultural Univeristy, Coimbatore-3, India).

Introduction. Much of the widely adapted wheat germ plasm generated and distributed by CIMMYT throughout the spring wheat production areas in low latitude countries carry a T1BL·1RS translocation. The wheat-breeding community has relied particularly on the use of the *Sr31* gene derived from wheat-rye hybrid derivatives produced in Germany in the 1930s (Metten et al. 1973; Zeller 1973) that gave continued protection against stem rust worldwide. The T1BL·1RS segment carries genes for resistance to three rusts, *Sr31*, *Lr26*, and *Yr9*, and *Pm8* for resistance to powdery mildew (Zeller 1973). However, in many genetic backgrounds, especially wheat lines of CIMMYT origin, the expression of *Pm8* is suppressed by a gene(s) located in chromosome 1A (Ren et al. 1997) or 7D (Zeller et al. 1993). In addition, the translocation may contribute positively to agronomic traits such as yield and drought tolerance (Rajaram et al. 1983). On the negative side, wheat lines with the translocation generally produce lower quality flour than their non-T1BL·1RS counterparts (Dhaliwal et al. 1987), indicating that the rye genes present are responsible for low gluten quality.

Singh et al. (1990) used SDS-PAGE to examine the genetic linkage between the genes controlling secalins (*Sec-1*) and those for resistance to the three rust diseases. The rust resistance genes are located 5.4±1.7 cM from the *Sec-1* locus, suggesting a close linkage (Afshari 2006). Because of the lack of pairing between the wheat and rye chromatin (IB and T1BL·1RS) in a wheat background, *Sec-1* acts as a marker for *Sr31*, *Lr26*, *Yr9*, and *Pm8*.

The ineffectiveness of *Sr31* against the new stem rust race Ug99 (Singh et al. 2004, 2006), which threatens wheat grain production worldwide, offers much hope to diversify the genetic base of the cultivar by pyramiding effective genes with or without *Sr31*.

The six Indian popular wheat cultivars, HD 2329, HD 2285, HP 1205, WH 147, J 24, and Lok-1, already with *Sr24+Lr24* that were introgressed with the *Sr31* gene complex through conventional backcross methods, were obtained for the confirmation of the presence of *Sr31*.

For the molecular analysis, protein was extracted using a protein-extraction buffer and separated in a vertical dual-gel unit (Sigma-Aldrich). Electrophoresis was at a constant 30 mA or until the bromophenol blue dye migrated to 1.5–2 cm above the gel base. SDS-PAGE used Laemmli (1970) buffer. The gel was then rinsed with distilled water and destained in 10% (v/v) acetic acid and 30% (v/v) methanol for 20 minutes, followed by washing in distilled water for 50 minutes with gentle shaking. The protein bands were documented on a digital gel documentation unit. The data on phenotyping of the constituted lines was done at IARI, Regional Station, Wellington.

Results and discussion. The SDS-PAGE procedure revealed patterns of water-soluble proteins that detected the T1BL·1RS translocation in wheat cultivars. The SDS-PAGE results showed that all the wheat stocks introgressed with the *S. cereale*-derived, linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8*, HW 4042 (HD 2329 with *Lr28*), HW 4044 (Lok-1 with *Lr28*), HW 4047 (WH 147 with *Lr28*), HW 4049 (HD 2285 with *Lr28*), and HW 4062 (J 24 with *Lr28*), carried the *Sec-1* band and the presence of the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* thus confirming the T1BL·1RS translocation. The recurrent parent HP 1205 also with the *Sr31* gene complex shows the *Sec-1* band. The protein bands corresponded to the secalins of the rye parent, which were present in the wheat cultivars carrying T1B·1R translocation. The *Sec-1* band was not found in the recurrent parents HD 2329, HD 2285, WH 147, J 24, and Lok-1, which do not have *Sr31* and suggesting the absence of the T1B·1R translocation. The lines pyramided with *T. ponticum*-derived linked genes *Lr24+Sr24*, and the *S. cereale*-derived gene complex are expected to yield better than the recurrent parent under field conditions.

The phenotyping data (Table 2) showed that the recurrent parents HW 2037, HW 2036, HW 2032, and HW 2033 (all carrying the *Ae. speltoides*-derived leaf rust resistance gene *Lr28*) were highly susceptible to all stem and stripe rusts, except HW

Table 2. Adult-plant response to black (Sr), brown (Lr), and yellow (Yr) rust and powdery mildew (Pm, 0–4 scale) diseases in wheat genotypes that carry specific rust-resistance genes and their recurrent parents.

Stock	Back-ground of recurrent parent	Genes	Adult-plant response			
			Sr	Lr	Yr	Pm
HW 2037	HD 2329	<i>Lr28</i>	90S	F	90S	2
HW 4042	HD 2329	<i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , <i>Pm8</i> , and <i>Lr28</i>	10R–MR	F	F	3
HW 2038	HD 2285	<i>Lr28</i>	50MS–S	F	30S	2
HW 4049	HD 2285	<i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , <i>Pm8</i> , and <i>Lr28</i>	10R–MR	F	F	3
HW 2036	J 24	<i>Lr28</i>	90S	F	100S	2
HW 4062	J 24	<i>Sr25</i> , <i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , <i>Pm8</i> , and <i>Lr28</i>	20R–MR	F	F	4
HW 2032	Lok-1	<i>Lr28</i>	90S	F	80S	3
HW 4044	Lok-1	<i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , <i>Pm8</i> , and <i>Lr28</i>	15R–MR	F	F	3
HW 2033	WH 147	<i>Lr28</i>	100S	F	90S	2
HW 4047	WH 147	<i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , <i>Pm8</i> , and <i>Lr28</i>	15R–MR	F	F	3
HW 4444	HP 1205	<i>Sr25+Lr19</i>	30MS–S	F	90S	4
	HP 1205	<i>Sr25+Lr19</i> , <i>Sr31</i> , <i>Lr26</i> , <i>Yr9</i> , and <i>Pm8</i>	F	F	F	3

2038, which was attributed to the presence of the *Sr8+Sr9b+Sr11* gene complex. However, HW 4444 in the background of HP 1205 showed resistance to leaf and stem rust because of the presence of *Lr19+Sr25*. The stocks HW 4042, HW 4049, HW 4062, HW 4044, HW 4047, and HW 4444 with *Sr31*, *Lr26*, *Yr9*, and *Pm8* from *S. cereale* clearly showed remarkable resistance against all three rusts. The *Sec-1* band clearly demonstrates and confirms that these lines carry *S. cereale*-derived, *Sr31*+gene complex.

Because *Sec-1* is tightly linked with the three rust resistance genes, SDS-PAGE is a useful method to identify and confirm the presence of rye chromatin and the three genes. The protein marker band associated with *Sec-1* is 5.4 ± 1.7 cM from the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* and can be exploited for detecting the T1RS·1BL translocation and developing lines with or without the *Sr31* gene complex (Fig 1.). Because *Sr31* is not effective against the emerging threat posed by the Ug99 stem rust pathotype and associated with poor gluten quality, this technique can be used to select lines without *Sr31*. *Sec-1* can be introgressed with other effective stem rust resistance genes such as *Sr24* (virulent pathotype 40-1 already reported from India), *Sr25*, *Sr26*, or *Sr27* for developing cultivars that produce better quality flour. Otherwise, *Sec-1* can be pyramided with other effective stem rust gene(s) to exploit the positive yield traits associated with the *Sr31* gene complex. The *Sec-1* marker will be a quick and economical method for screening large numbers of wheat germ plasm lines for the presence of *Sr31* in the laboratory without any greenhouse facility in a short period of time.

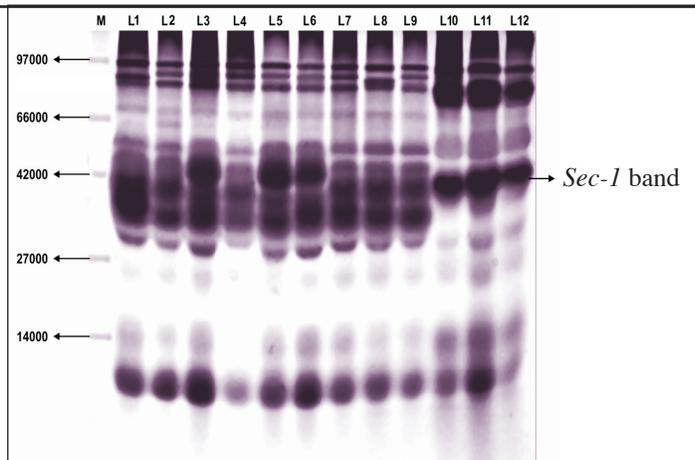


Fig. 1. Banding patterns of seed protein extracts from wheat stocks and various controls subjected to SDS-PAGE electrophoresis (lanes L to R: M, marker (14–97 Kda); L1, HW 4444 (+); L2, WH 542 (donor) (+); L3, HW 4049 (+); L4, HW4042 (+); L5, HW 2038 (rye parent) (-); L6, HW 2037 (Recurrent parent) (-); L7, HW 4062 (+); L8, HW 4044 (+); L9, HW 4047 (+); L10, R-1 (+); L11, R-2 (+); and L12, R-4 (+). The presence or absence of the Sec-1 band the presence or absence of T1BL·1RS is indicated by (+) and (-), respectively.

References.

- Afshari F. 2006. Protein marker assisted identification of *Yr9*, *Lr26* and *Sr31* genes in a group of Iranian wheat cultivars. *J Agric Sci Technol* 8:265-268.
- Dhaliwal HS, Mares DJ, and Marshall DR. 1987. Effect of the 1BL·1RS translocation on milling and quality characteristics of bread wheats. *Cereal Chem* 64:72-76.
- Laemmli UK. 1970. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* 227:680-685.
- Menon MK and Tomar SMS. 2007. Introgression of petkus rye chromatin into wheat. *Ind J Agric Sci* 77(2):92-95.
- Mettin D, Bluthner WD, and Schlegel G. 1973. Additional evidence on spontaneous 1B·1R wheat-rye substitutions and translocations. *In: Proc 4th Internat Wheat Genet Symp* (Sears LMS and Sears ER, Eds). University of Missouri, Colombia, U.S. Pp. 179-184.
- Rajaram S, Mann CE, Ortiz-Ferrara G, and Mujeeb-Kazi A. 1983. Adaptation, stability and high yield potential of certain 1B·1R CIMMYT wheat. *In: Proc 6th Internat Wheat Genet Symp* (Sakamoto S, Ed). Plant Germ-Plasm Insitute, Kyoto.Japan. Pp. 613-621.
- Ren SX, McIntosh RA, and Lu ZJ. 1997. Genetic suppression of the cereal-rye derived gene *Pm8* in wheat. *Euphytica* 93:353-360.
- Singh NK, Shepherd KW, and McIntosh RA. 1990. Linkage mapping of genes for resistance to leaf, stem and stripe rusts and *Sec-1* on the short arm of rye chromosome 1R. *Theor Appl Genet* 80:609-616.

Developing elite, durable disease resistant wheat cultivars combining high grain yield and end-use quality by introgressing effective genes employing conventional and modern breeding approaches.

M. Sivasamy, Jagdish Kumar, M.K. Menon and S.M.S. Tomar (Division of Genetics, Indian Agricultural Research Institute, New Delhi).

Introduction. A meticulously planned, wheat-improvement program employing back-cross methodology to introgress effective rust and powdery mildew resistance genes was initiated during late eighties and early nineties. Popular Indian bread wheat and dicoccum wheat cultivars were used. The reference stocks (RILs) obtained were initially evaluated for resistance, and only effective genes conferring resistance to existing pathotypes were taken for the program. The effec-

tive resistance genes were introgressed initially through a conventional back-cross hybridization method taking advantage of Wellington where in all three rusts and other foliar diseases occur on a susceptible line throughout the year and is considered as natural 'hot spot'. Later, when markers were made available, both conventional and MAS approaches are used. Initially, the number of backcrosses effected were 8–9, but now we stop with BC₃. For molecular confirmation, the mapping populations were used at the BC₁F₂ stage.

Alien rust-resistance genes in the back-cross program at IARI, Wellington (Table 3, p. 89).

Stem rust resistance genes:	<i>Sr2</i> (linked to pseudo-black chaff (<i>Pbc</i>)), <i>Sr22</i> , <i>Sr24</i> , <i>Sr25</i> , <i>Sr26</i> , <i>Sr27</i> (linked to apical claw on spike), <i>Sr29</i> , <i>Sr30</i> , <i>Sr31</i> , <i>Sr32</i> , <i>Sr33</i> , <i>Sr35</i> , <i>Sr36</i> , <i>Sr38</i> , <i>Sr39</i> , <i>Sr42</i> , and <i>Sr43</i> .
Leaf rust resistance genes:	<i>Lr9</i> (not effective in India), <i>Lr19</i> (new virulence reported), <i>Lr24</i> , <i>Lr26</i> (not effective in India), <i>Lr28</i> , <i>Lr32</i> , <i>Lr34</i> (adult-plant resistance (APR) is race nonspecific and linked to leaf tip necrosis), <i>Lr35</i> (APR), <i>Lr37</i> , <i>Lr39</i> , <i>Lr40</i> , <i>Lr41</i> , <i>Lr42</i> , <i>Lr45</i> (linked to pink awn/glume at milk stage under low temperature), <i>Lr46</i> (APR, race nonspecific), <i>Lr47</i> , <i>Lr48</i> , <i>Lr49</i> , <i>Lr53</i> , and <i>Lr57</i> .
Stripe rust resistance genes:	<i>Yr9</i> , <i>Yr10</i> , <i>Yr15</i> , <i>Yr16</i> , <i>Yr17</i> , <i>Yr18</i> , <i>Yr24</i> , <i>Yr25</i> , <i>Yr26</i> , <i>Yr29</i> , <i>Yr30</i> , <i>Yr35</i> , and <i>Yr40</i> .
Powdery mildew resistance genes:	<i>Pm6</i> , <i>Pm8</i> , <i>Pm38</i> , and <i>Pm39</i>

Pleiotropic or closely linked to genes (race nonspecific) exploited that are effective to other diseases include *Lr34/Yr18/Pm38/Bdv1/Sr resistance/Ltn*, *Lr46/Yr29/Pm39/Ltn*, and *Sr2/Yr30/(Lr27)/Pbc*.

Linked genes that are exploited include *Lr19+Sr25*, *Lr24+Sr24*, *Yr30+Sr2+Lr27*, *Lr26*+Yr9+Sr31+Pm8*, *Lr37*+Yr17+Sr38*, and *Sr39+Lr35*.

Pyramiding of effective stem rust-resistance genes currently under progress to overcome threat from Ug99 and its variants of stem rust race virulent on *Sr31*, *Sr24*, and *Sr36* virulence spectrum of Ug99 (TTKSK). Genes that currently are effective against Ug99 are *Sr25* (*Lophopyrum ponticum*); *Sr28*¹, *Sr29*², and *SrTmp*¹ (*T. aestivum* subsp. *aestivum*); *Sr2*, *Sr13*^{1,2}, and *Sr14*¹ (*T. turgidum* subsp. *turgidum*); *Sr22* and *Sr35* (*T. monococcum* subsp. *monococcum*); *Sr36*¹ and *Sr37* (*T. timopheevii* subsp. *timopheevii*); *Sr32* and *Sr39* (*Ae. speltoides*); *Sr33*² and *Sr45* (*Ae. tauschii*); *Sr40* (*T. timopheevii* subsp. *armeniicum*); *Sr26* and *Sr43* (*Th. elongatum*); *Sr44* (*Th. intermedium*); and *Sr27*¹ and *Sr1A·1R*¹ (*S. cereale*). For genes marked with a ¹, virulence for the gene is known to occur in other races; for those with a ², the level of resistance conferred in the field usually insufficient (Singh et al 2008).

Markers available in public domain used at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stem rust: *Sr1A*, *Sr2*, *Sr9a*, *Sr11*, *Sr13*, *Sr14*, *Sr15*, *Sr17*, *Sr19*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr28*, *Sr29*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr37*, *Sr38*, *Sr39*, *Sr40*, *Sr43*, *Sr44*, *Sr45*, *Sr46*, *SrR*, *SrTmp*, *SrTt3*, and *SrD5*; leaf rust: *Lr19*, *Lr24*, *Lr28*, *Lr32*, *Lr35*, *Lr37*, *Lr39*, *Lr26*, *Lr47*, *Lr50*, and *Lr51*; and yellow rust: *Yr9*, *Yr10*, *Yr15*, *Yr17*, *Yr18*, *Yr26*, and *Yr28* (Bariana et al. 2007).

Accomplishments.

- Combinations of *Sr24+Sr25*, *Sr25+Sr26*, *Sr25+Sr27*, *Sr25+Sr36*, *Sr25+Sr38*, *Sr24+Sr26*, *Sr24+Sr27*, and *Sr24+Sr36* are pyramided with *Yr10* in at least 20 adapted Indian bread wheat cultivars and the material is ready for sharing. Even stocks with *Lr19+Sr25+Sr36+Pm6* and *Yr15*, which are free from leaf, stem, and stripe rusts and powdery mildew have been developed and published (Table 4, pp. 90-91).
- Popular Indian bread wheat cultivars with *Lr24+Sr24* and *Lr19+Sr25* along with *Sr36+Pm6*, *Lr28*, and *Lr37* developed in 20 cultivar backgrounds have been completed and published.
- Corrective crosses for *Lr19+Sr25* where Sunstar was used are using 'wheatear'.
- Corrective crosses for *Lr32* (Thatcher *Lr32*) also is in progress at the BC₃F₂ stage.
- Incorporated of new leaf rust genes *Lr35+Sr39* (during Kharif 2010), *Lr39* (BC₃), *Lr42*, *Lr44*, *Lr45* (at BC₃F₃ stage) in 28 popular Indian bread wheat cultivars.
- Current efforts to incorporate/pyramid *Lr46*, *Lr47*, *Lr48*, and *Lr57* in combination with *Yr10* and *Yr15*.
- Pyramiding of *Sr24* with *Sr31*, *Lr19+Sr25* with *Sr31*, and *Lr19+Sr25* with *Lr24+Sr24* completed in 20 popular cultivars and published.
- *Lr28*, *Lr32*, and *Lr37* with *Sr36+Pm6* in 20 popular cultivars complete.

Table 3. Effective rust-resistance genes used in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington (* reference stock attributes are listed in Table 4, pp. 90-91).

Gene	Source	Reference stock used*	Chromosome location
Lr9 (ineffective at Wellington since 1995)	<i>Ae. umbellulata</i>	Abe	6BL
Lr19+Sr25, Sr36+Pm6 (77-8 race reported in Peninsular Zone, India, during 2008)	<i>Th. ponticum</i>	Sunstar and Cook and now wheatear	7DL
Lr24+Sr24 (40-1 race reported in Wellington on Sr24)	<i>Th. ponticum</i>	Tr380-14*7/3Ag#14 Janz, Sunleg, RL6064, Agent	3DL
Lr26+Sr31+Yr9+Pm8 (77-1 race reported from Wellington for Lr26)	<i>S. cereale</i> (Petkus rye)	WH 542 (Bucanora)	T1BL1RS
Lr28	<i>Ae. speltoides</i>	CS 2A/2M 4/2	4AL
Lr32	<i>Ae. tauschii</i>	C86-8/KalyansonaF ₄ / Thatcher Lr32	3DS
Lr34+Yr18+BDV1 Pm38+Sr resistance/Ltn (APR race nonspecific)	<i>T. aestivum</i> subsp. <i>aestivum</i> cultivar Terenizo	RL6058	7DS
Lr35+Sr39	<i>Ae. speltoides</i>	Thatcher+Lr35	2B
Lr37+Sr38+Yr17	<i>Ae. ventricosa</i>	Thatcher*8/VPM1, RL6081	2AS
Lr39	<i>Ae. tauschii</i>	KS92WGRC15, EZ 350692	2DS
Lr40	<i>Ae. tauschii</i>	LC+Lr40, KS89WGRC07	1D
Lr41	<i>Ae. tauschii</i>	EC381200, KS90WGRC10	2DS
Lr42	<i>Ae. tauschii</i>	EC381201, KS91WGRC11	1D
Lr44	<i>T. aestivum</i> subsp. <i>spelta</i>	EC381202, RL6147	1BL
Lr45	<i>S. cereale</i> (Imperial rye)	EC 381203, RL6144	TAS-2R
Lr46	<i>T. aestivum</i> subsp. <i>aestivum</i>	Pavon 76, Dimond Bird	1BL
Lr47	<i>Ae. speltoides</i>	Pavon 7 S3 Lr47, KS90H450	7AS
Sr2+Lr27+Yr30+Pbc (pseudo-black chaff)	<i>T. aestivum</i> subsp. <i>aestivum</i>	Maden, Lok-1, HW 5207	3BS
Sr22 (APR)	<i>T. monococcum</i> subsp. <i>monococcum</i>		7AL
Sr24	<i>Th. ponticum</i>	Tr380-14*7/3Ag#14	3DL
Sr25+Lr19+Sr36+Pm6	<i>Th. ponticum</i>		7DL
Sr26	<i>Th. ponticum</i>	DARF*6/3Ag3/Kite	6AL
Sr27	<i>S. cereale</i> (Imperial rye)	Kalyansona*4/Sr27	3A
Sr29	<i>T. aestivum</i> subsp. <i>aestivum</i>	Pusa 4/Etoile de choisy	6DL
Sr30	<i>T. aestivum</i> subsp. <i>aestivum</i>	BtSr30Wst	5DL
Sr32	<i>Ae. speltoides</i>	CnsSr32 AS	2A, 2B, 2AS
Sr33	<i>Ae. tauschii</i>	RL5405	1DL, 1DS
Sr35	<i>T. monococcum</i> subsp. <i>monococcum</i>	Mq(2)/5*G2919	3AL
Sr36+pm6	<i>T. timopheevii</i> subsp. <i>timopheevii</i>	Cook*6/C 80-1	2BS
Sr38	<i>Ae. ventricosa</i>	Thatcher*8/VPM1, RL6081	2AS
Sr39	<i>Ae. speltoides</i> (APR)	Thatcher+Lr35	2B
Sr42	<i>T. aestivum</i> subsp. <i>aestivum</i>	EC381206	6DS
Sr43	<i>Th. ponticum</i>	EC381210	7DL
Sr44	<i>Th. ponticum</i>		7AS?, 7DS
Yr10	<i>T. aestivum</i> subsp. <i>spelta</i>	Moro, Yr10+WH 542	1BS
Yr15	<i>T. turgidum</i> subsp. <i>dicoccoides</i>	<i>T. dicoccoides</i> G-25	1BL
Yr16	Capelle-Desprez	Capelle-Desprez	2DS
Yr17	<i>Ae. ventricosa</i>	Thatcher*8/VPM1, RL6081	2AS
Pm6	<i>T. timopheevii</i> subsp. <i>timopheevii</i>	Cook*6/C 80-1, Abe	2BS

Table 4. *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
Abe	<i>Lr9 Sr36</i> (Not effective in India)	15R MR	F	40S	1
Sunstar*6/C80-1 (molecularly confirmed not carrying <i>Lr19</i> , 'wheatear' used now)	<i>Lr19 Sr25</i>	10R MR–30R MR	F	F	4
	<i>Lr19+Sr25</i>	F	F	10MR–MS	3
Cook*6/C 80-1	<i>Lr19 Sr25 Sr36 Pm6</i>	F	F	F	1
Tr380-14*7/3Ag#14	<i>Lr24 Sr24</i> (<i>Sr24</i> not effective in India)	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	<i>Lr24 Sr24 Sr26</i>	10R MR–20R MR	F	10MS	3
WH 542	<i>Lr26</i> (not effective in India) <i>Sr31 Yr9 Pm8</i>	10R MR	80S	F	3
CS 2A/2M 4/2	<i>Lr28 Sr34 Yr8</i>	90S	F	F	0–1
C86-8/Kalyansona F ₄ (not carrying <i>Lr32</i> ; Thatcher <i>Lr32</i> used now)	<i>Lr32</i>	70S	F	90S	3
	<i>Lr32</i>	60S	F	20S	2
RL6058	<i>Lr 34 Yr18 BDV1 Pm38</i>	F	30MR–MS	F	0–1
Thatcher+ <i>Lr 35</i>	<i>Lr35</i> (Race specific APR) <i>Sr39</i>	F	F	F	2
Thatcher*8/VPM1, RL6081	<i>Lr37 Sr38 Yr17</i>	20R MR MS	F	15MS	4
KS92WGRC15, EZ350692	<i>Lr39</i>	40S	F	F	2
LC+ <i>Lr40</i>	<i>Lr40</i>	S	S	F	2
EC381200	<i>Lr41</i>	5S	F	30S	3
EC381201	<i>Lr42</i>	F	F	40S	3
KS92WGRC16	<i>Lr43</i>	F	F	40S	2
EC381202	<i>Lr44</i>	20S	20S	F	2
EC381203	<i>Lr45</i>	S	F	S	3
Pavon 76	<i>Lr46</i>		20MS		
Pavon	<i>Lr47</i>	F	F	10S	2
Tr380-14*7/3Ag#14	<i>Sr24 Lr24</i>	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	<i>Sr24 Sr26 Lr24</i>	10R MR–20R MR	F	10MS	3
Sunstar*6/C80-1 (molecularly confirmed not carrying <i>Lr19</i> , 'wheatear' used now)	<i>Sr25 Lr19</i>	10R MR–30R MR	F	F	4
Cook*6/C 80-1	<i>Sr25 Sr36 Lr19 Pm6</i>	F	F	F	1
Kalyanasona*4/Sr27	<i>Sr27</i>	F–Tr	80S	90S	3
Pusa 4/Etoile de Choisy	<i>Sr 29</i>	F			
BtSr30Wst	<i>Sr 30</i>	F			
WH 542	<i>Sr31 Lr26 Yr9 Pm8</i>	10R MR	80S	F	3
CnsSr 32 AS	<i>Sr 32</i>	F			
RL5405	<i>Sr33</i>	F			
CS 2A/2M 4/2	<i>Sr34</i>	90S	F	F	0–1
Mq(2)/5*G2919	<i>Sr35</i>	F			
Abe	<i>Sr36</i>	15R MR	F	40S	1
	<i>Sr37</i>	F	80S	30S	2
Thatcher*8/VPM 1,RL 6081	<i>Sr38</i>	20R MR MS	F	15MS	4

Table 4 (continued). *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
EC381198	<i>Sr38</i>	F	F	F	4
Thatcher+ <i>Lr35</i>	<i>Sr39</i>	F	F	F	2
EC381204	<i>Sr39</i>	F	F	F	2
RL6087	<i>Sr40</i>	F	60S	F	2
EC381206	<i>Sr42</i>	F	40S	5S	2
EC381210	<i>Sr43</i>	F	80S	F	1
CS 2A/2M 4/2	<i>Yr8 Lr28 Sr34</i>	90S	F	F	0-1
WH 542	<i>Yr9 Lr26 Sr31 Pm8</i>	10R MR	80S	F	3
Moro, WH 542	<i>Yr10</i>	F	F	F	0-1
<i>T. dicocoides</i> G-25	<i>Yr15</i>	F	F	F	0-1
Capelle-Desprez	<i>Yr16</i>	F	F	F	0-1
Thatcher*8/VPM1, RL6081	<i>Yr17 Lr37 Sr38</i>	20R MR MS	F	15MS	4
EC463655	<i>Yr17</i>	F	90S	F	NA
EC463057	<i>Yr24</i>	F	40S	20S	NA
EC463658	<i>Yr26</i>	F	20S	30S	NA

Table 5. Number wheat cultivars released for commercial use developed through the alien gene backcross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Cultivar	Pedigree	Year of release	Release target zone
HW 2004 (Amar)	C 306//Tr 380-14*7//3 Ag # 14	1997	Central zone, rainfed
HW 1085 (Bhavani)	HW 2002A//CPAN 3057	1998	Southern Hill Zone, medium fertility, timely sown
HW 2044 (Kurinji)	PBW 226*5//Sunstar*6/C 80 -1	2000	Southern Hill Zone, medium fertility, timely sown
HW 2045 (Kaushambi)	HD2402*5//Sunstar*6/C80-1	2003	North Eastern Plain Zone, late sown
HS 375 (HIMGIRI) (In collaboration)	BB/G11/CJ 71/3/TAEST//KAL/BB	2003	Northern Hill Zone, very high altitude, timely sown
HS 420 (Shivalik) (In collaboration)	RAJ3302//cmh 73a-49*7/3*CNO 79	2003	Northern Hill Zone, late sown
HD 2833 (In collaboration)	PBW 226/HW 1042 (Tr 380-14*7/3 Ag#14)// HD 2285	2005-06	Peninsular Zone
MACS 6145 (HW 2034) (In collaboration)	C 306*9//CS 2A/2M*4/2	2004	North Eastern Plain Zone, rainfed
COW(W) 1 (HW 3094) (In collaboration)	HD 2646//HW 2002A/CPAN 3057	2004	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)
HW 5207 (Pusa Nava-giri)	HW 3029// <i>Yr15</i>	2009-10	Southern Hill Zone, medium fertility, timely sown
Hw 1095 as CoW(SW)2 (Dicoccum)	NP200 - Mutant through Gamma Irradiation (y)(200 Gray)	2010	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)

Targeted breeding program to tackle the Ug99 threat accomplishments.

- Introgression of pyramided genes involving *Sr2* and *Sr22* with *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr29*, *Sr30*, *Sr33*, *Sr35*, *Sr36*, and *Sr44* in at least 20 important, currently popular cultivars across the zones is under progress, many

Table 6. *Triticum aestivum* subsp. *aestivum* recurrent parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s) already carrying	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew (0–4 scale)
C 306	<i>Lr34+Yr18+BDV1+Pm38+Sr</i> resistance/ <i>Ltn</i> (unknown resistance gene for yellow rust)	90S	90S	F	3
HD 2009		40S	60S	100S	3
HD 2285	<i>Lr23+Sr9b+Sr11+Yr2</i>	30MS	100S	30S	3
HD 2329	<i>Lr13+Lr10+Lr34, Sr8+Sr9b+Sr11+Yr2+Yr18</i>	80S	90S	90S	3
HD 2402	<i>Lr34+</i> unknown resistance gene for yellow rust	30S	100S	F	3
HD 2687	<i>Sr31 Lr26 Yr9 Pm8</i>	15R MR	80S	F	3
HI 1077	<i>Lr14a</i>	30MS S	50S	40S	3
HS 240	<i>Sr31 Lr26 Yr9 Pm8</i>	5R MR	70S	F	3
HUW 234	<i>Lr14a+Sr9b+Sr11+Yr2+(Ks)</i> and <i>Sr31 Lr26 Yr9 Pm8</i>	20MS S	100S	F	3
J 24		90S	100S	100S	3
Kalyansona	<i>Yr2</i>	80S	90S	90S	3
Lok-1	<i>Lr13+Sr2+Sr9b+Sr11+Yr18</i>	70S	80S	80S	3
NI 5439	<i>Lr34+Yr18+BDV1+Pm38+Sr</i> resistance/ <i>Ltn</i> and <i>Sr11+Yr2</i>	90S	90S	100S	3
PBW 226		20S	90S	F	3
Sonalika	<i>Lr11</i> and <i>Lr13</i> (Gupta et al. 1984; Rao et al. 2001)	60S	80S	60S	3
UP 262		50S	50S	50S	3
UP 2338	<i>Lr26+Lr34+Sr31+Yr9+Yr18</i>	10MR	60S	F	3
VL 421		60S	90S	80S	3
WH 147	<i>Lr34</i>	90S	90S	90S	3
WH 542	<i>Lr34, Sr31 Lr26 Yr9 Pm8</i>	10R MR	80S	F	3
WL 711	<i>Lr11</i> and <i>Lr13</i> (Gupta et al. 1984; Rao et al. 2001)	100S	100S	90S	3
HI 977		F	60S	40S	2
HP 1205		60SS	80SS	90S	3
PBN 51		20MR	40S	S	2
PBW 343	<i>Lr34</i>	20MR	60S	5S	3
Raj 3077		5MR	60SS	60SS	1
HD 2877	<i>Sr31</i>	5MR	40SS	F	3
HW 3070	<i>Lr24+Sr24, Sr31</i>	F	F	10MR-10S	2
HD 2733	<i>Sr31</i>	20MR	60S	F	3

- at BC₂ stage in Rabi 2009–10.
- Simultaneous molecular confirmations are under taken
- More than 400 near isogenic lines carrying various specific rust resistance genes developed.

Some salient observations made on the introgression lines with above-mentioned rust resistance genes.

- *Lr24+Sr24* are tightly linked, but new pathotype virulent on *Sr24* (40-1/62G29) was reported from this station.
- *Sr31*, *Lr26*, *Yr9*, and *Pm8* are tightly linked and linked to slow senescence of leaf and high susceptibility to powdery mildew. A new pathotype virulent on *Lr26* (77-5) was reported from Wellington, *Pm8* is ineffective in a spring wheat back ground, the virulent races available at Wellington were showing 5MR–MS reaction to yellow rust, *Sr31* gave a 20MR–MS reaction.
- *Lr28* and *Lr32* were observed to be associated with fast rusting to stem rust susceptibility and a reduced level of infection to powdery mildew, *Lr28* and *Lr32* have association with fast rusting to stem rust.
- *Lr24+Sr24* and *Sr27* are associated with phenotypical markers of apical claw on the spike.
- *Lr19+sr25* seems to be associated with slow leaf senescence and increased yield, however, the susceptibility level for powdery mildew increases.
- *Lr37+Sr28+Yr17* introgression not giving yellow rust resistance in all backgrounds indicating the existence of certain suppressor genes at that particular loci.
- *Sr31* is associated with red grain, in derivatives there is always a chance to get amber grains.

Table 7. Maintenance and utilization of wild species of wheat at the Indian Agricultural Research Institute, Regional Station, Wellington, under this program 2009–09.

Species	Gene pool	Genome	Ploidy level (2n)	Total accessions
<i>Ae. biuncialis</i>	Tertiary	UM	28	122
<i>Ae. columanaris</i>	Tertiary	U ^{co} M ^{co}	28	17
<i>Ae. comosa</i>	Tertiary	M	14	3
<i>Ae. comosa</i> var. <i>comosa</i>	Tertiary	M	14	1
<i>Ae. comosa</i> var. <i>subventricosa</i>	Tertiary	M	14	1
<i>Ae. crassa</i>	Secondary	DJ, DJX	28, 42	9
<i>Ae. cylindrica</i>	Secondary	CD	28	75
<i>Ae. geniculata</i>	Tertiary	U ^s M ^s	28	110
<i>Ae. juvenalis</i>	Secondary	DMU	42	1
<i>Ae. kotschyii</i>	Tertiary	USS	28	9
<i>Ae. longissima</i>	Secondary	SB	14	36
<i>Ae. markgrafii</i>	Tertiary	CC	14	39
<i>Ae. neglecta</i>	Tertiary	UM	28	102
<i>Ae. peregrina</i>	Tertiary	US	28	55
<i>Ae. peregrina</i> var. <i>brachythera</i>	Tertiary	US	28	3
<i>Ae. peregrina</i> var. <i>peregrina</i>	Tertiary	US	28	1
<i>Ae. searsii</i>	Secondary	SS	14	50
<i>Ae. sharonensis</i>	Secondary	S ^{sh}	14	77
<i>Ae. speltoides</i>	Secondary	S	14	29
<i>Ae. speltoides</i> var. <i>ligustica</i>	Secondary	S	14	9
<i>Ae. speltoides</i> var. <i>speltoides</i>	Secondary	S	14	6
<i>Ae. tauchii</i>	Primary	D	14	81
<i>Ae. triuncialis</i>	Tertiary	UC	28	239
<i>Ae. triuncialis</i> var. <i>persica</i>	Tertiary	U ^c	28	2
<i>Ae. umbellulata</i>	Tertiary	U	14	52
<i>Ae. uniaristata</i>	Tertiary	Mt	14	2
<i>Ae. ventricosa</i>	Secondary	D ^v N ^v	28	1
<i>T. monococcum</i> subsp. <i>aegilopoides</i>	Primary	A ^m	14	742
<i>T. timopheevii</i> subsp. <i>armeniicum</i>	Secondary	AG	28	252
<i>T. timopheevi</i> subsp. <i>timopheevii</i>	Secondary	AG	28	22
<i>T. turgidum</i> subsp. <i>dicoccoides</i>	Primary	AB	28	595
<i>T. urartu</i>	Primary	A		171
<i>Secale cereale</i>	Tertiary	R	14, 16, 20	136
Total accessions				2,938
Total from tertiary gene pool				155

- *Yr9* is ineffective in a spring wheat background.
- *Lr45* seems to be linked to pink awn and glumes at milk stage under low temperature.
- *Lr32* and *Lr28* in combination with *Sr31* are observed to give enhanced yield, to be investigated and exploited.
- *Lr35* and *Lr45* seems to not enhancing the yield and need further investigation.
- *Lr45* can easily be selected for based on pink awn color.
- Combinations of major and minor genes pyramided in certain elite cultivars is the long-term solution.
- *Lr19* and *Sr31* seem to be associated with high susceptibility to powdery mildew.
- *Lr45* seems to be associated with lax spikes although fertility in the lowest spikelet is restored.

Other externally funded projects in operation now at IARI, Regional Station, Wellington include 1. a DBT-funded Net work project 'Molecular Marker Assisted development of biotic stress resistant wheat varieties' and 2. an Indo-Australian breeding program on 'Molecular markers for broadening the genetic base of stem rust resistance genes effective against strain Ug99'.

References

- Bariana HS, Brown GN, Bansal UK, Miah H, Standen GE, and Lu M. 2007. Breeding triple rust resistant wheat cultivars for Australia using conventional and marker-assisted selection technologies. *Aus J Agric Res* 58:576-587.
- Gupta AK, Saini RG, Gupta S, and Malhotra S. 1984. Genetic analysis of two wheat cultivars, 'Sonalika' and 'WL 711' for reaction to leaf rust (*Puccinia recondita*). *Theor Appl Genet* 67(2-3):215-217.
- Rao S, Singh G, and Chatterjee M. 2001. Indian Wheat Pool. *In: The World Wheat Book, A History of Wheat Breeding* (Bonjean AP and Angus WJ, Eds). Lavoisier Publishers, Paris, France. Pp. 773-816.
- Singh RP, Hodson DP, Huerta-Espino J, Jin Y, Njau P, Wanyera R, Herrera-Foessel SA, Bhavani S, Singh D, and Singh PK. 2008. Global status of Ug99 spread and efforts to mitigate the threat. *In: Proc Internat Conf 'Wheat Stem Rust Ug99 – A Threat to Food Security* (Singh GP, Prabhu KV, and Singh AM, Eds). *Ind Agric Res Inst, New Delhi, India*. P. 85.
- Singh RP, Huerta-Espino J, Pfeiffer W, and Figueroa-Lopez P. 2004. Occurrence and impact of a new leaf rust race on durum wheat in northwestern Mexico from 2001 to 2003. *Plant Dis* 88:703-708.
- Singh RP, Kinyua MG, Wanyera R, Njau P, Jin Y, and Huerta-Espino J. 2007. Spread of a highly virulent race of *Puccinia graminis tritici* in eastern Africa: challenges and opportunities. *In: Wheat Production in Stressed Environments, Proc 7th Internat Wheat Conf, Mar del Plata, Argentina* (Buck HT, Nisi JE, and Salomón N, Eds). Springer, the Netherlands. Pp. 51-57.
- Zeller FJ. 1973. 1B·1R wheat-rye chromosome substitutions and translocations. *In: Proc Fourth Internat Wheat Genet Symp* (Sears ER and Sears LMS, Eds). University of Missouri, Columbia, US. Pp. 209-221.
- Zeller FJ, Lutz J, and Stephan U. 1993. Chromosome location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L.) 1. *Mlk* and other alleles at the *Pm3* locus. *Euphytica* 68:223-229.

Ug99 virulence of wheat stem rust pathogen yet not detected in India.

J. Kumar and M. Sivasamy.

The virulence of race Ug99 of *Puccinia graminis* Pers..f.sp. *tritici* Eriks. & E.Henn. causing stem rust of wheat was recognized first in Uganda during 1999. Ug99 has the potential of migrating into India as documented by other rust races migrating from eastern Africa to southern Asia. A huge area in India is under cultivation of the mega-cultivar PBW 343 and other Veery cultivars with the gene *Sr31*, which has been rated to be highly susceptible when tested in Kenya (Singh et al. 2006). Owing to the inherent capability of stem rust spores for wind dispersal for long distances, the Nilgiri Hills in Tamil Nadu the state of South India are one of the prospective Indian targets of Ug99 virulence. A continuous vigil thus becomes imperative for tracking the supposed introduction of Ug99 and variants at this location, especially because wheat and stem rust survives here throughout the year.

The Wellington Station of the Indian Agricultural Research Institute situated in the Nilgiri Hills of Tamil Nadu in India is an ideal place to undertake Ug99 surveillance because stem rust survives here in vivo on wheat grown year round as winter and summer (off-season) crops. This IARI research station is well prepared to track the field incidence (if it happens) of new pathogenic strains such as Ug99 with a battery of well-maintained greenhouses for accomplishing virulence analysis in wheat rust pathogens. A quick, differential set comprising wheat lines capable of capturing Ug99

and its variants is regularly planted in a staggered way with repeating sowing at three-month intervals to maintain adult-stage plants continuously in the field. The quick set is comprised of the wheat lines Morocco (no *Sr* gene), LMPG (no *Sr* gene), Seri-MACS 2496, Bacanora-WH 542, Attila-PBW 343, *Sr31*/LMPG, *Sr24* (Tr 380-14), *Sr36* (Cook-2), *Sr36* (Cook), and *Sr36* (LMPG).

In the month of November 2009, the quick set also was planted at all regional stations of IARI; Shimla (North Hill zone), the Wheat Division of IARI headquarters in Delhi (North Western Plain Zone), Indore (Central Zone), and Wellington (South Hill Zone). These stations cover all the agro-ecological situations in India suitable for wheat cultivation. Uredospore dust was collected from 146 leaf samples of stem rust from the premises of the IARI Regional Station, Wellington, between April 2009 and April 2010 from the regular winter (March–April 2009 and October 2009–April 2010) and the summer crops (July–November, 2009). Seedlings of the quick set were inoculated and seedling reactions recorded following Bahadur et al. (1985). These samples yielded only the existing Indian pathotypes and none resembled Ug99 or its reported variants. The adult-stage reactions recorded in the first week of April, 2010, following the scale of Roelfs et al. (1992) indicated that all lines of the quick set were free of stem rust except Morocco, which was susceptible at Indore and Wellington. We have concluded that Ug99 has not yet reached in Nilgiri Hills or other parts of India so far.

References.

- Roelfs AP, Singh RP, and Saari EE. 1992. Rust diseases of wheat: concepts and methods of disease management. CIMMYT Mexico, D.F. 81 pp.
- Bahadur P, Nagarajan S, and Nayar SK. 1985. Proc Ind Acad Sci 95:29-33.
- Singh RP, Hodson DP, Jin Y, Huerta-Espino J, Kinyua MG, Wanyera R, Njau P, and Ward RW. 2006. Current status, likely migration and strategies to mitigate the threat to wheat production from race Ug99 (TTKS) of stem rust pathogen, <http://www.cabi.org/cabreviews/default.aspx?LoadModule=Review&ReviewID=25637&site=167&page=1178>.

ITEMS FROM ITALY

CONSIGLIO PER LA RICERCA E LA SPERIMENTAZIONE IN AGRICOLTURA, Unità di ricerca per la valorizzazione qualitativa dei cereali (CRA-QCE), Via Cassia, 176, 00191 Rome, Italy.

Pyramiding of leaf rust-resistance genes in common wheat using marker-assisted selection.

F. Nocente, L. Gazza, L. Sereni, and M. Pasquini.

Foliar diseases, such as leaf rust caused by *Puccinia triticina* Eriks. (*Pt*), have been important factors limiting wheat production worldwide. This pathogen is regarded as potentially the most damaging causal agent of rust disease on wheat in Italy, where it is widespread and needs constant monitoring.

One strategy for increasing the durability of resistance in commercial cultivars is to pyramid multiple resistance genes into a single wheat genotype. Pyramiding two or more genes, irrespective of whether they are major or minor, with different modes of action can greatly delay or even prevent the breakdown of resistance. The introgression of two or more genes into the same genetic background is difficult to monitor by traditional phenotypic analysis alone because of the epistatic or dominance effects of some genes or the lack of pathotypes with virulences matching the corresponding resistance gene(s). The availability of specific molecular markers tightly linked to respective resistance genes makes the detection of multiple genes in one genotype possible; such markers are the basis for efficient marker-assisted selection (MAS) in breeding work to speed up the identification of lines carrying two or more resistance genes.

Several known genes for resistance to leaf rust, often derived from related species and genera, have confirmed their efficacy in Italy over a long period. Epidemiological field controls in different locations in Italy and greenhouse